

SEQUENCE LISTING

<110> Smith, Michael D.
Potter, Robert Jason
Dhariwal, Gulshan
Gerard, Gary F.
Rosenthal, Kim
Lee, Jun

<120> Thermostable Reverse Transcriptases and Uses Thereof

<130> 0942.5040003

<150> US 60/410,283
<151> 2002-09-13

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<170> PatentIn version 3.2

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Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys His
20 25 30
atg acc cta aat ata gaa gat gag tat cgg cta cat gag acc tca aaa 144
Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys
35 40 45
gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag 192
Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
50 55 60
gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct 240
Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
65 70 75 80
ctg atc ata ctt ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa 288
Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
85 90 95
tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag 336
Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
100 105 110

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Arg	Leu	Leu	Asp	Gln	Gly	Ile	Leu	Val	Pro	Cys	Gln	Ser	Pro	Trp	Asn	
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acg	ccc	ctg	cta	ccc	gtc	aag	aaa	ccc	ggg	act	aat	gat	tac	agg	cct	432
Thr	Pro	Leu	Leu	Pro	Val	Lys	Lys	Pro	Gly	Thr	Asn	Asp	Tyr	Arg	Pro	
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Val	Gln	Asp	Leu	Arg	Glu	Val	Asn	Lys	Arg	Val	Glu	Asp	Ile	His	Pro	
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acc	gta	ccc	aac	ccc	tac	aac	ctc	ttg	agt	ggg	ctc	cca	ccg	tcc	cac	528
Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu	Pro	Pro	Ser	His	
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cag	tgg	tac	act	gtt	cta	gac	tta	aaa	gat	gcc	ttt	ttc	tgc	ctg	aga	576
Gln	Trp	Tyr	Thr	Val	Leu	Asp	Leu	Lys	Asp	Ala	Phe	Phe	Cys	Leu	Arg	
			180						185					190		
ctc	cac	ccg	acg	tct	cag	cct	ctc	ttc	gcc	ttt	gaa	tgg	aga	gac	cca	624
Leu	His	Pro	Thr	Ser	Gln	Pro	Leu	Phe	Ala	Phe	Glu	Trp	Arg	Asp	Pro	
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Phe	Lys	Asn	Ser	Pro	Thr	Leu	Phe	Asp	Glu	Ala	Leu	Arg	Arg	Asp	Leu	
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Asp	Asp	Leu	Leu	Leu	Ala	Ala	Thr	Ser	Glu	Leu	Asp	Cys	Gln	Gln	Gly	
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Thr	Arg	Ala	Leu	Leu	Gln	Thr	Leu	Gly	Asp	Leu	Gly	Tyr	Arg	Ala	Ser	
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Val	Met	Gly	Gln	Pro	Thr	Pro	Lys	Thr	Pro	Arg	Gln	Leu	Arg	Glu	Phe	
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cta act gcc cca gcc ctg ggg ttg cca gat ttg act aag ccc ttt gaa Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu 385 390 395 400			1200
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cat atc cat gga gaa ata tac aga agg cgt ggg ttg ctc aca tca gaa	1920
His Ile His Gly Glu Ile Tyr Arg Arg Arg Gly Leu Leu Thr Ser Glu	
625 630 635 640	
ggc aaa gag atc aaa aat aag gac gag ata ttg gcc cta cta aaa gcc	1968
Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala	
645 650 655	
ctc ttt ctg ccc aaa aga ctt agc ata atc cat tgt cca gga cat caa	2016
Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln	
660 665 670	
aag gga cac agc gcc gag gct aga ggc aac cgg atg gct gac caa gcg	2064
Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala	
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gcc cga aag gca gcc atc aca gag aat cca gac acc tct acc ctc ctc	2112
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690 695 700	
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<213> Artificial Sequence

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<223> Mutant Reverse Transcriptase Derived from Moloney Murine Leukemia Virus

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35 40 45

Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
50 55 60

Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro
65 70 75 80

Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln
85 90 95

Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln
100 105 110

Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn
115 120 125

Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro
130 135 140

Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro
145 150 155 160

Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His
165 170 175

Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg
180 185 190

Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro
195 200 205

Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly
210 215 220

Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu
225 230 235 240

Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val
245 250 255

Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly
260 265 270

Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser
275 280 285

Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr
290 295 300

Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr
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Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe
325 330 335

Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu

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Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu 420 425 430		
Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala 435 440 445		
Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro 450 455 460		
Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro 465 470 475 480		
Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu 485 490 495		
Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn 500 505 510		
Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys 515 520 525		
Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp 530 535 540		
Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser 545 550 555 560		
Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu 565 570 575		
Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln 580 585 590		

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Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly
595 600 605

Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala
610 615 620

His Ile His Gly Glu Ile Tyr Arg Arg Arg Gly Leu Leu Thr Ser Glu
625 630 635 640

Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala
645 650 655

Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln
660 665 670

Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala
675 680 685

Ala Arg Lys Ala Ala Ile Thr Glu Asn Pro Asp Thr Ser Thr Leu Leu
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Ile Glu Asn Ser Ser Pro Asn Ser Arg Leu Ile Asn
705 710 715

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gctaysacca tgattacgns caagcytgca tgctgcagg tcgactctag aggatccccg      180
ggtaccgagc tcgaattyac tggycgtcgt tntwacaacg tcgtgwctgg gaanaaccct      240
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